

C. Koutman

1646

#13

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/878,168ADATE: 02/23/1999
TIME: 14:30:00

Input Set: H878168A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Ashkenazi, Avi J.
2 Baker, Kevin
3 Gurney, Austin
4 Wood, William
5 <120> TITLE OF INVENTION: Apo-2DcR
6 <130> FILE REFERENCE: 11669.29US02
7 <140> CURRENT APPLICATION NUMBER: US/08/878,168A
8 <141> CURRENT FILING DATE: 1997-06-18
9 <160> NUMBER OF SEQ ID NOS: 17
10 <170> SOFTWARE: FastSEQ for Windows Version 3.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 259
13 <212> TYPE: PRT
14 <213> ORGANISM: HUMAN
15 <400> SEQUENCE: 1
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17 1 5 10 15
18 Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu
19 20 25 30
20 Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe
21 35 40 45
22 Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly
23 50 55 60
24 Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
25 65 70 75 80
26 Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
27 85 90 95
28 His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln Cys Lys
29 100 105 110
30 Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys Arg Lys Cys
31 115 120 125
32 Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
33 130 135 140
34 Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu
35 145 150 155 160
36 Thr Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala
37 165 170 175
38 Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro
39 180 185 190
40 Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala
41 195 200 205
42 Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
43 210 215 220
44 Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr

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45      225      230      235      240
46      Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile
47      245      250      255
48      Val Phe Val
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58      gtttgaccag agatgcaagg ggtgaaggag cgcttcctac cgttagggaa ctctggggac      120
59      agagcgcccc ggccgcctga tggccgagggc aggggtgcgac ccaggaccca ggacggcgtc      180
60      gggaaccata cc atg gcc cgg atc ccc aag acc cta aag ttc gtc gtc gtc      231
61      Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val
62      1      5      10
63      atc gtc gcg gtc ctg ctg cca gtc cta gct tac tct gcc acc act gcc      279
64      Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala
65      15      20      25
66      cgg cag gag gaa gtt ccc cag cag aca gtg gcc cca cag caa cag agg      327
67      Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
68      30      35      40      45
69      cac agc ttc aag ggg gag gag tgt cca gca gga tct cat aga tca gaa      375
70      His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu
71      50      55      60
72      cat act gga gcc tgt aac ccg tgc aca gag ggt gtg gat tac acc aac      423
73      His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn
74      65      70      75
75      gct tcc aac aat gaa cct tct tgc ttc cca tgt aca gtt tgt aaa tca      471
76      Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser
77      80      85      90
78      gat caa aaa cat aaa agt tcc tgc acc atg acc aga gac aca gtg tgt      519
79      Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys
80      95      100      105
81      cag tgt aaa gaa ggc acc ttc cgg aat gaa aac tcc cca gag atg tgc      567
82      Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys
83      110      115      120      125
84      cgg aag tgt agc agg tgc cct agt ggg gaa gtc caa gtc agt aat tgt      615
85      Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn Cys
86      130      135      140
87      acg tcc tgg gat gat atc cag tgt gtt gaa gaa ttt ggt gcc aat gcc      663
88      Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala
89      145      150      155
90      act gtg gaa acc cca gct gct gaa gag aca atg aac acc agc ccg ggg      711
91      Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly
92      160      165      170
93      act cct gcc cca gct gct gaa gag aca atg aac acc agc cca ggg act      759
94      Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr

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95      175      180      185
96      cct gcc cca gct gct gaa gag aca atg acc acc agc ccg ggg act cct      807
97      Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro
98      190      195      200      205
99      gcc cca gct gct gaa gag aca atg acc acc agc ccg ggg act cct gcc      855
100     Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala
101     210      215      220
102     cca gct gct gaa gag aca atg acc acc agc ccg ggg act cct gcc tct      903
103     Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser
104     225      230      235
105     tct cat tac ctc tca tgc acc atc gta ggg atc ata gtt cta att gtg      951
106     Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val
107     240      245      250
108     ctt ctg att gtg ttt gtt tgaagactt cactgtggaa gaaattcctt      999
109     Leu Leu Ile Val Phe Val
110     255
111     ccttacctga aaggttcagg taggcgctgg ctgagggcgg ggggcgctgg acactctctg      1059
112     ccctgcctcc ctctgctgtg ttcccacaga cagaaacgcc tgcccctgcc ccaaaaaaaaa      1119
113     aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1179
114     a      1180
115     <210> SEQ ID NO 3
116     <211> LENGTH: 299
117     <212> TYPE: PRT
118     <213> ORGANISM: HUMAN
119     <400> SEQUENCE: 3
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121     1      5      10      15
122     Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
123     20      25      30
124     Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro Lys Thr Leu
125     35      40      45
126     Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr
127     50      55      60
128     Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
129     65      70      75      80
130     Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly
131     85      90      95
132     Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
133     100     105     110
134     Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys
135     115     120     125
136     Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr
137     130     135     140
138     Arg Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
139     145     150     155     160
140     Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val
141     165     170     175
142     Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu
143     180     185     190
144     Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met

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145          195          200          205
146  Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn
147          210          215          220
148  Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
149          225          230          235          240
150  Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser
151          245          250          255
152  Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro
153          260          265          270
154  Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
155          275          280          285
156  Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
157          290          295
158 <210> SEQ ID NO 4
159 <211> LENGTH: 1180
160 <212> TYPE: DNA
161 <213> ORGANISM: HUMAN
162 <220> FEATURE:
163 <221> NAME/KEY: CDS
164 <222> LOCATION: (73)...(969)
165 <221> NAME/KEY: sig_peptide
166 <222> LOCATION: (73)...(194)
167 <400> SEQUENCE: 4
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169  gtttgaccag ag atg caa ggg gtg aag gag cgc ttc cta ccg tta ggg aac      111
170          Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn
171          -40          -35          -30
172  tct ggg gac aga gcg ccc cgg cgg cct gat ggc cga ggc agg gtg cga      159
173  Ser Gly Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg
174          -25          -20          -15
175  ccc agg acc cag gac ggc gtc ggg aac cat acc atg gcc cgg atc ccc      207
176  Pro Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
177          -10          -5          1          5
178  aag acc cta aag ttc gtc gtc gtc atc gtc gcg gtc ctg ctg cca gtc      255
179  Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val
180          10          15          20
181  cta gct tac tct gcc acc act gcc cgg cag gag gaa gtt ccc cag cag      303
182  Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro Gln Gln
183          25          30          35
184  aca gtg gcc cca cag caa cag agg cac agc ttc aag ggg gag gag tgt      351
185  Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys
186          40          45          50
187  cca gca gga tct cat aga tca gaa cat act gga gcc tgt aac ccg tgc      399
188  Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys
189          55          60          65
190  aca gag ggt gtg gat tac acc aac gct tcc aac aat gaa cct tct tgc      447
191  Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys
192          70          75          80          85
193  ttc cca tgt aca gtt tgt aaa tca gat caa aaa cat aaa agt tcc tgc      495
194  Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys

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195		90		95		100		
196	acc atg acc aga gac aca gtg tgt cag tgt aaa gaa ggc acc ttc cgg							543
197	Thr Met Thr Arg Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg							
198		105		110		115		
199	aat gaa aac tcc cca gag atg tgc cgg aag tgt agc agg tgc cct agt							591
200	Asn Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser							
201		120		125		130		
202	ggg gaa gtc caa gtc agt aat tgt acg tcc tgg gat gat atc cag tgt							639
203	Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys							
204		135		140		145		
205	gtt gaa gaa ttt ggt gcc aat gcc act gtg gaa acc cca gct gct gaa							687
206	Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu							
207		150		155		160		165
208	gag aca atg aac acc agc ccg ggg act cct gcc cca gct gct gaa gag							735
209	Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu							
210		170		175		180		
211	aca atg aac acc agc cca ggg act cct gcc cca gct gct gaa gag aca							783
212	Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr							
213		185		190		195		
214	atg acc acc agc ccg ggg act cct gcc cca gct gct gaa gag aca atg							831
215	Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met							
216		200		205		210		
217	acc acc agc ccg ggg act cct gcc cca gct gct gaa gag aca atg acc							879
218	Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr							
219		215		220		225		
220	acc agc ccg ggg act cct gcc tct tct cat tac ctc tca tgc acc atc							927
221	Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile							
222		230		235		240		245
223	gta ggg atc ata gtt cta att gtg ctt ctg att gtg ttt gtt							969
224	Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val							
225		250		255				
226	tgaaagactt cactgtggaa gaaattcctt ccttacctga aagggttcagg taggcgctgg							1029
227	ctgagggcgg ggggcgctgg acactctctg ccctgcctcc ctctgctgtg ttcccacaga							1089
228	cagaaacgcc tgcccctgcc ccaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa							1149
229	aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a							1180
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231	<211> LENGTH: 43							
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233	<213> ORGANISM: YEAST							
234	<400> SEQUENCE: 5							
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237	<211> LENGTH: 41							
238	<212> TYPE: DNA							
239	<213> ORGANISM: YEAST							
240	<400> SEQUENCE: 6							
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242	<210> SEQ ID NO 7							
243	<211> LENGTH: 49							
244	<212> TYPE: PRT							

Please Note:

Use 'n' and/or 'Xaa' have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> <223> fields of each sequence which presents at least one 'n' or 'Xaa'.

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text

423 W "N" or "Xaa" used: Feature required

Tyr Leu Glu Gly Asn Ala Asp Ser Ala Xaa S